

DI-12  
SEQUENCE LISTING

<110> Weber, Eric R.  
Jensen, Wayne A.  
Chandrashekar, Ramaswamy

<120> CANINE TAg1 PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF

<130> DI-12

<140> not yet assigned

<141> 2001-07-30

<150> 60/224,655

<151> 2000-08-11

<160> 85

<170> PatentIn version 3.1

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cgatgactac agaggatgct tggacctgaa gttggaggag ctgaaatcct ttgttctgcc 480  
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&lt;223&gt; n = unknown at position 1111

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Glu Gln Pro Arg Gly Pro Gly Gly Ala Glu Arg Gly Gly Ser Glu Leu
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ggc gac gcg ggc gca gcg ggg cag ctg aac cct tgg aac ata atg ata      150
Gly Asp Ala Gly Ala Ala Gly Gln Leu Asn Pro Trp Asn Ile Met Ile
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aag cac agg cag gtg cag cga agg ggc cgc cgc tca cag atg aca aca      198
Lys His Arg Gln Val Gln Arg Arg Gly Arg Arg Ser Gln Met Thr Thr
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agt ttc aca gat cct gcc att tcc atg gac ctc ctt cga gct gtc ctg      246
Ser Phe Thr Asp Pro Ala Ile Ser Met Asp Leu Leu Arg Ala Val Leu
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cag cct agc atc aac gag gag atc cag acg gtc ttc aac aag tat atg      294
Gln Pro Ser Ile Asn Glu Glu Ile Gln Thr Val Phe Asn Lys Tyr Met
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aag ttc ttc cag aag gca gca ctg aac gtc aga gac aat gtc ggg gaa      342
Lys Phe Phe Gln Lys Ala Ala Leu Asn Val Arg Asp Asn Val Gly Glu
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Glu Val Asp Ala Glu Gln Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu
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gag cag gct aaa ctc ctg ttt tca gat gga gaa aaa gta ata ccc aga      438
Glu Gln Ala Lys Leu Leu Phe Ser Asp Gly Glu Lys Val Ile Pro Arg
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Leu Ala His Glu Leu Pro Gly Ile Lys Arg Gly Arg Gln Thr Glu Glu
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Trp Lys Pro Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp
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gac cca gcc cgg ctg aat gaa tct acc acc ttt gtg ttg gga tct cga      678
Asp Pro Ala Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser Arg
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gcc aac aag gcc ctg ggg atg ggg ggc acc aga ggg aga atc tac atc      726
Ala Asn Lys Ala Leu Gly Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile
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aag cac ccg cac ctc ttt aag tat gca gct gac ccc cag gac aag cac      774
Lys His Pro His Leu Phe Lys Tyr Ala Ala Asp Pro Gln Asp Lys His
      235                      240                      245

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Trp Leu Ala Glu Gln His His Met Arg Ala Thr Gly Gly Lys Met Ala
      250                      255                      260

tac ctc ctc atc gag gag gac atc cgg gac ctc gca gcc agt gat gac      870
Tyr Leu Leu Ile Glu Glu Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp
      265                      270                      275

tat aga gga tgc ctg gac ttg aag ttg gag gag ctg aaa tcc ttt gtg      918
Tyr Arg Gly Cys Leu Asp Leu Lys Leu Glu Glu Leu Lys Ser Phe Val
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ctg ccc tcc tgg atg gtt gag aag atg cga aag tac atg gag aca cta      966
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Arg Thr Glu Asn Glu His Arg Ala Val Glu Ala Pro Pro Gln Thr
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ctgggctagt ctgtagtac tcactacaga gcacccccag actggcgtgt ggttctgttt      1191

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<213> Canis familiaris

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DI-12

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35 40 45

Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala Ile Ser Met  
50 55 60

Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu Glu Ile Gln  
65 70 75 80

Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala Ala Leu Asn  
85 90 95

Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln  
100 105 110

Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu Phe Ser Asp  
115 120 125

Gly Glu Lys Val Ile Pro Arg Leu Ala His Glu Leu Pro Gly Ile Lys  
130 135 140

Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala His Arg Gly Ser Pro Val  
145 150 155 160

Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Met Leu Ser Asn Asp  
165 170 175

Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys Glu Pro Ile  
180 185 190

Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn Glu Ser Thr  
195 200 205

Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly Met Gly Gly  
210 215 220

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Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe Lys Tyr Ala  
225 230 235 240

Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His His Met Arg  
245 250 255

Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu Asp Ile Arg  
260 265 270

Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp Leu Lys Leu  
275 280 285

Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val Glu Lys Met  
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Glu Ala Pro Pro Gln Thr  
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gctganatcc atccaggtgc agtcccagca gtggcctccg ccacgtgggt gccagggcct 180  
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ttcaacagca cgatgctcgt tctctgtccg tagtgtctcc atgtactttc gcatcttctc 300  
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 tggaagctca tgggccaatc tgggtattac tttttctcca tctgaaaaca ggagtttagc 840  
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 gag cgg ggc ggc tcc gag ctg ggc gac gcg ggc gca gcg ggg cag ctg 96  
 Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
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 aac cct tgg aac ata atg ata aag cac agg cag gtg cag cga agg ggc 144  
 Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln Arg Arg Gly  
 35 40 45  
 cgc cgc tca cag atg aca aca agt ttc aca gat cct gcc att tcc atg 192  
 Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala Ile Ser Met  
 50 55 60  
 gac ctc ctt cga gct gtc ctg cag cct agc atc aac gag gag atc cag 240  
 Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu Glu Ile Gln  
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Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln	
100 105 110	
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Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu Phe Ser Asp	
115 120 125	
gga gaa aaa gta ata ccc aga ttg gcc cat gag ctt cca ggg ata aag	432
Gly Glu Lys Val Ile Pro Arg Leu Ala His Glu Leu Pro Gly Ile Lys	
130 135 140	
cgt ggc cga cag aca gaa gag gaa tgt gcc cat cga gga agc cct gtt	480
Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala His Arg Gly Ser Pro Val	
145 150 155 160	
ccc aaa aag agg aaa gga cgg cct cct gga cac atg ctg tcg aat gac	528
Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Met Leu Ser Asn Asp	
165 170 175	
cgg gca gcc gct ggc atg gta tgg aaa cca aag tcc tgt gaa cca att	576
Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys Glu Pro Ile	
180 185 190	
cgc cga gaa ggc ccc aag tgg gac cca gcc cgg ctg aat gaa tct acc	624
Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn Glu Ser Thr	
195 200 205	
acc ttt gtg ttg gga tct cga gcc aac aag gcc ctg ggg atg ggg ggc	672
Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly Met Gly Gly	
210 215 220	
acc aga ggg aga atc tac atc aag cac ccg cac ctc ttt aag tat gca	720
Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe Lys Tyr Ala	
225 230 235 240	
gct gac ccc cag gac aag cac tgg ctg gcc gag cag cat cac atg cgg	768
Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His His Met Arg	
245 250 255	
gca aca ggg ggg aag atg gcc tac ctc ctc atc gag gag gac atc cgg	816
Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu Asp Ile Arg	
260 265 270	
gac ctc gca gcc agt gat gac tat aga gga tgc ctg gac ttg aag ttg	864
Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp Leu Lys Leu	
275 280 285	
gag gag ctg aaa tcc ttt gtg ctg ccc tcc tgg atg gtt gag aag atg	912
Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val Glu Lys Met	
290 295 300	
cga aag tac atg gag aca cta cgg aca gag aac gag cat cgt gct gtt	960

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 Glu Ala Pro Pro Gln Thr  
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978

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 35 40 45

Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala Ile Ser Met  
 50 55 60

Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu Glu Ile Gln  
 65 70 75 80

Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala Ala Leu Asn  
 85 90 95

Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln  
 100 105 110

Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu Phe Ser Asp  
 115 120 125

Gly Glu Lys Val Ile Pro Arg Leu Ala His Glu Leu Pro Gly Ile Lys  
 130 135 140

Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala His Arg Gly Ser Pro Val  
 145 150 155 160

Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Met Leu Ser Asn Asp  
 165 170 175



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Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys Glu Pro Ile  
180 185 190

Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn Glu Ser Thr  
195 200 205

Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly Met Gly Gly  
210 215 220

Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe Lys Tyr Ala  
225 230 235 240

Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His His Met Arg  
245 250 255

Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu Asp Ile Arg  
260 265 270

Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp Leu Lys Leu  
275 280 285

Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val Glu Lys Met  
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 gag cgg ggc ggc tcc gag ctg ggc gac gcg ggc gca gcg ggg cag ctg 96  
 Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
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Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln Arg Arg Gly  
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 Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu Glu Ile Gln  
           20                          25                          30  
 acg gtc ttc aac aag tat atg aag ttc ttc cag aag gca gca ctg aac 144  
 Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala Ala Leu Asn  
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 Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln  
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<212> PRT  
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Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala Ala Leu Asn  
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Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln  
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gaccgtctgg atctcctcgt tgatgctagg ctgcaggaca gctcgaagga ggtccatgga 180  
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gag ctt cca ggg ata aag cgt ggc cga cag aca gaa gag gaa tgt gcc 96  
Glu Leu Pro Gly Ile Lys Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala

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cac atg ctg tcg aat gac cgg gca gcc gct ggc atg gta tgg aaa cca His Met Leu Ser Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro 50 55 60			192
aag tcc tgt gaa cca att cgc cga gaa ggc ccc aag tgg gac cca gcc Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala 65 70 75 80			240
cgg ctg aat gaa tct acc acc ttt gtg ttg gga tct cga gcc aac aag Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys 85 90 95			288
gcc ctg ggg atg ggg ggc acc aga ggg aga atc tac atc aag cac ccg Ala Leu Gly Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro 100 105 110			336
cac ctc ttt aag tat gca gct gac ccc cag gac aag cac tgg ctg gcc His Leu Phe Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala 115 120 125			384
gag cag cat cac atg cgg gca aca ggg ggg aag atg gcc tac ctc ctc Glu Gln His His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu 130 135 140			432
atc gag gag gac atc cgg gac ctc gca gcc agt gat gac tat aga gga Ile Glu Glu Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly 145 150 155 160			480
tgc ctg gac ttg aag ttg gag gag ctg aaa tcc ttt gtg ctg ccc tcc Cys Leu Asp Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser 165 170 175			528
tgg atg gtt gag aag atg cga aag tac atg gag aca cta cgg aca gag Trp Met Val Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu 180 185 190			576
aac gag cat cgt gct gtt gaa gcg cct cca cag acc Asn Glu His Arg Ala Val Glu Ala Pro Pro Gln Thr 195 200			612

<210> 15  
 <211> 204  
 <212> PRT  
 <213> Canis familiaris  
  
 <400> 15

Lys Leu Leu Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala His  
 1 5 10 15

## DI-12

Glu Leu Pro Gly Ile Lys Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala  
 20 25 30

His Arg Gly Ser Pro Val Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly  
 35 40 45

His Met Leu Ser Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro  
 50 55 60

Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala  
 65 70 75 80

Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys  
 85 90 95

Ala Leu Gly Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro  
 100 105 110

His Leu Phe Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala  
 115 120 125

Glu Gln His His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu  
 130 135 140

Ile Glu Glu Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly  
 145 150 155 160

Cys Leu Asp Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser  
 165 170 175

Trp Met Val Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu  
 180 185 190

Asn Glu His Arg Ala Val Glu Ala Pro Pro Gln Thr  
 195 200

<210> 16  
 <211> 612  
 <212> DNA  
 <213> Canis familiaris

<400> 16  
 ggtctgtgga ggcgcttcaa cagcacgatg ctcgttctct gtccgtagtg tctccatgta 60  
 ctttcgcata ttctcaacca tccaggaggg cagcacaaag gatttcagct cctccaactt 120

DI-12

caagtccagg catcctctat agtcatcact ggctgcgagg tcccggatgt cctcctcgat 180  
gaggaggtag gccatcttcc cccctgttgc ccgcatgtga tgctgctcgg ccagccagtg 240  
cttgtcctgg gggtcagctg cataactaaa gaggtgctgg tgcttgatgt agattctccc 300  
tctggtgccc cccatcccca gggccttggt ggctcgagat cccaacacaa aggtggtaga 360  
ttcattcagc cgggctgggt cccacttggg gccttctcgg cgaattgggt cacaggactt 420  
tggtttccat accatgccag cggctgcccg gtcattcgac agcatgtgtc caggaggccg 480  
tcctttcctc tttttgggaa cagggttcc tcgatgggca cattcctctt ctgtctgtcg 540  
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aaacaggagt tt 612

<210> 17  
<211> 1269  
<212> DNA  
<213> Canis familiaris  
  
<220>  
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<222> (58)..(1044)  
<223>

<400> 17  
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atg ggg gcc act ggc gac gcc gag cag ccg cgg gga ccc ggc ggg gca 105  
Met Gly Ala Thr Gly Asp Ala Glu Gln Pro Arg Gly Pro Gly Gly Ala  
1 5 10 15  
  
gag cgg ggc ggc tcc gag ctg ggc gac gcg ggc gca gcg ggg cag ctg 153  
Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
20 25 30  
  
gta ctc acg aac cct tgg aac ata atg ata aag cac agg cag gtg cag 201  
Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln  
35 40 45  
  
cga agg ggc cgc cgc tca cag atg aca aca agt ttc aca gat cct gcc 249  
Arg Arg Gly Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala  
50 55 60  
  
att tcc atg gac ctc ctt cga gct gtc ctg cag cct agc atc aac gag 297  
Ile Ser Met Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu  
65 70 75 80  
  
gag atc cag acg gtc ttc aac aag tat atg aag ttc ttc cag aag gca 345  
Glu Ile Gln Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala  
85 90 95  
  
gca ctg aac gtc aga gac aat gtc ggg gaa gaa gtg gac gca gag cag 393

## DI-12

Ala	Leu	Asn	Val	Arg	Asp	Asn	Val	Gly	Glu	Glu	Val	Asp	Ala	Glu	Gln		
			100					105					110				
ctg	atc	cag	gag	gcc	tgt	cgg	agc	tgc	ctg	gag	cag	gct	aaa	ctc	ctg	441	
Leu	Ile	Gln	Glu	Ala	Cys	Arg	Ser	Cys	Leu	Glu	Gln	Ala	Lys	Leu	Leu		
		115					120					125					
ttt	tca	gat	gga	gaa	aaa	gta	ata	ccc	aga	ttg	gcc	cat	gag	ctt	cca	489	
Phe	Ser	Asp	Gly	Glu	Lys	Val	Ile	Pro	Arg	Leu	Ala	His	Glu	Leu	Pro		
	130					135					140						
ggg	ata	aag	cgt	ggc	cga	cag	aca	gaa	gag	gaa	tgt	gcc	cat	cga	gga	537	
Gly	Ile	Lys	Arg	Gly	Arg	Gln	Thr	Glu	Glu	Glu	Cys	Ala	His	Arg	Gly		
145					150					155					160		
agc	cct	gtt	ccc	aaa	aag	agg	aaa	gga	cgg	cct	cct	gga	cac	atg	ctg	585	
Ser	Pro	Val	Pro	Lys	Lys	Arg	Lys	Gly	Arg	Pro	Pro	Gly	His	Met	Leu		
				165					170					175			
tcg	aat	gac	cgg	gca	gcc	gct	ggc	atg	gta	tgg	aaa	cca	aag	tcc	tgt	633	
Ser	Asn	Asp	Arg	Ala	Ala	Ala	Gly	Met	Val	Trp	Lys	Pro	Lys	Ser	Cys		
			180					185					190				
gaa	cca	att	cgc	cga	gaa	ggc	ccc	aag	tgg	gac	cca	gcc	cgg	ctg	aat	681	
Glu	Pro	Ile	Arg	Arg	Glu	Gly	Pro	Lys	Trp	Asp	Pro	Ala	Arg	Leu	Asn		
		195					200					205					
gaa	tct	acc	acc	ttt	gtg	ttg	gga	tct	cga	gcc	aac	aag	gcc	ctg	ggg	729	
Glu	Ser	Thr	Thr	Phe	Val	Leu	Gly	Ser	Arg	Ala	Asn	Lys	Ala	Leu	Gly		
	210					215					220						
atg	ggg	ggc	acc	aga	ggg	aga	atc	tac	atc	aag	cac	ccg	cac	ctc	ttt	777	
Met	Gly	Gly	Thr	Arg	Gly	Arg	Ile	Tyr	Ile	Lys	His	Pro	His	Leu	Phe		
225					230					235					240		
aag	tat	gca	gct	gac	ccc	cag	gac	aag	cac	tgg	ctg	gcc	gag	cag	cat	825	
Lys	Tyr	Ala	Ala	Asp	Pro	Gln	Asp	Lys	His	Trp	Leu	Ala	Glu	Gln	His		
				245				250						255			
cac	atg	cgg	gca	aca	ggg	ggg	aag	atg	gcc	tac	ctc	ctc	atc	gag	gag	873	
His	Met	Arg	Ala	Thr	Gly	Gly	Lys	Met	Ala	Tyr	Leu	Leu	Ile	Glu	Glu		
			260					265					270				
gac	atc	cgg	gac	ctc	gca	gcc	agt	gat	gac	tat	aga	gga	tgc	ctg	gac	921	
Asp	Ile	Arg	Asp	Leu	Ala	Ala	Ser	Asp	Asp	Tyr	Arg	Gly	Cys	Leu	Asp		
		275					280					285					
ttg	aag	ttg	gag	gag	ctg	aaa	tcc	ttt	gtg	ctg	ccc	tcc	tgg	atg	gtt	969	
Leu	Lys	Leu	Glu	Glu	Leu	Lys	Ser	Phe	Val	Leu	Pro	Ser	Trp	Met	Val		
	290					295					300						
gag	aag	atg	cga	aag	tac	atg	gag	aca	cta	cgg	aca	gag	aac	gag	cat	1017	
Glu	Lys	Met	Arg	Lys	Tyr	Met	Glu	Thr	Leu	Arg	Thr	Glu	Asn	Glu	His		
305					310					315					320		
cgt	gct	gtt	gaa	gcg	cct	cca	cag	acc	tgaccgaagc	caagaccct						1064	
Arg	Ala	Val	Glu	Ala	Pro	Pro	Gln	Thr									
				325													



DI-12

ggctacactt ggcagccctc ctccaaggcc ctggcaccca cgtggcggag gccactgctg 1124  
 ggactgcacc tggatggatc tcagcagcat taagctgtgc ctgggctagt ctgtagtgac 1184  
 tcactacaga gcacccccag actggcgtgt gggtctgttt gtaaagttat cgggttaaga 1244  
 aacaattaaa cagtttttaa tagtg 1269

<210> 18  
 <211> 329  
 <212> PRT  
 <213> Canis familiaris

<400> 18

Met Gly Ala Thr Gly Asp Ala Glu Gln Pro Arg Gly Pro Gly Gly Ala  
 1 5 10 15

Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
 20 25 30

Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln  
 35 40 45

Arg Arg Gly Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala  
 50 55 60

Ile Ser Met Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu  
 65 70 75 80

Glu Ile Gln Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala  
 85 90 95

Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln  
 100 105 110

Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu  
 115 120 125

Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala His Glu Leu Pro  
 130 135 140

Gly Ile Lys Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala His Arg Gly  
 145 150 155 160

Ser Pro Val Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Met Leu

DI-12

165

170

175

Ser Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys  
180 185 190

Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn  
195 200 205

Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly  
210 215 220

Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe  
225 230 235 240

Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His  
245 250 255

His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu  
260 265 270

Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp  
275 280 285

Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val  
290 295 300

Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu Asn Glu His  
305 310 315 320

Arg Ala Val Glu Ala Pro Pro Gln Thr  
325

<210> 19  
<211> 1269  
<212> DNA  
<213> Canis familiaris

<400> 19  
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ccagtctggg ggtgctctgt agtgagtcac tacagactag cccaggcaca gcttaatgct 120  
gctgagatcc atccaggtgc agtcccagca gtggcctccg ccacgtgggt gccagggcct 180  
tgaggagggg ctgccaagtg tagccagggg tcttggtctc ggtcaggtct gtggaggcgc 240  
ttcaacagca cgatgctcgt tctctgtccg tagtgtctcc atgtactttc gcattctctc 300

## DI-12

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aaccatccag gagggcagca caaaggattt cagctcctcc aacttcaagt ccaggcatcc 360
tctatagtca tcaactggctg cgaggtcccg gatgtcctcc tcgatgagga ggtaggccat 420
cttccccctt gttgcccgca tgtgatgctg ctgggccagc cagtgttgt cctgggggtc 480
agctgcatac ttaaagaggt gcgggtgctt gatgtagatt ctccctctgg tgccccccat 540
ccccagggcc ttgttggtc gagatcccaa cacaaggtg gtagattcat tcagccgggc 600
tggttccac ttggggcctt ctggcgaat tggttcacag gactttggtt tccataccat 660
gccagcgggt gcccggtcat tcgacagcat gtgtccagga ggccgtcctt tcctcttttt 720
gggaacaggg ctctctgat gggcacattc ctctctgtc tgtcggccac gctttatccc 780
tggaagctca tgggccaatc tgggtattac ttttctcca tctgaaaaca ggagttagc 840
ctgctccagg cagctccgac aggcctcctg gatcagctgc tctgcgtcca ctctctcccc 900
gacattgtct ctgacgttca gtgtgcctt ctggaagaac ttcataact tgttgaagac 960
cgtctggatc toctcgttga tgctaggctg caggacagct cgaaggaggt ccatggaaat 1020
ggcaggatct gtgaaacttg ttgtcatctg tgagcggcgg ccccttcgct gcacctgcct 1080
gtgctttatc attatgttcc aagggttcgt gagtaccagc tgccccgctg cgcccgctc 1140
gccagctcg gagccgcccc gctctgcccc gccgggtccc cgcggctgct cggcgctgcc 1200
agtggcccc atggctcccc cggcgcccc caacctcagc ccgactctgc caccggccgg 1260
aaagtggcc 1269

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<210> 20
<211> 987
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(987)
<223>

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<400> 20
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Met Gly Ala Thr Gly Asp Ala Glu Gln Pro Arg Gly Pro Gly Gly Ala
1 5 10 15

gag cgg ggc ggc tcc gag ctg ggc gac gcg ggc gca gcg ggg cag ctg 96
Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu
20 25 30

gta ctc acg aac cct tgg aac ata atg ata aag cac agg cag gtg cag 144
Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln

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## DI-12

35	40	45	
cga agg ggc cgc cgc tca cag atg aca aca agt ttc aca gat cct gcc Arg Arg Gly Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala 50 55 60			192
att tcc atg gac ctc ctt cga gct gtc ctg cag cct agc atc aac gag Ile Ser Met Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu 65 70 75 80			240
gag atc cag acg gtc ttc aac aag tat atg aag ttc ttc cag aag gca Glu Ile Gln Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala 85 90 95			288
gca ctg aac gtc aga gac aat gtc ggg gaa gaa gtg gac gca gag cag Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln 100 105 110			336
ctg atc cag gag gcc tgt cgg agc tgc ctg gag cag gct aaa ctc ctg Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu 115 120 125			384
ttt tca gat gga gaa aaa gta ata ccc aga ttg gcc cat gag ctt cca Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala His Glu Leu Pro 130 135 140			432
ggg ata aag cgt ggc cga cag aca gaa gag gaa tgt gcc cat cga gga Gly Ile Lys Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala His Arg Gly 145 150 155 160			480
agc cct gtt ccc aaa aag agg aaa gga cgg cct cct gga cac atg ctg Ser Pro Val Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Met Leu 165 170 175			528
tcg aat gac cgg gca gcc gct ggc atg gta tgg aaa cca aag tcc tgt Ser Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys 180 185 190			576
gaa cca att cgc cga gaa ggc ccc aag tgg gac cca gcc cgg ctg aat Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn 195 200 205			624
gaa tct acc acc ttt gtg ttg gga tct cga gcc aac aag gcc ctg ggg Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly 210 215 220			672
atg ggg ggc acc aga ggg aga atc tac atc aag cac ccg cac ctc ttt Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe 225 230 235 240			720
aag tat gca gct gac ccc cag gac aag cac tgg ctg gcc gag cag cat Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His 245 250 255			768
cac atg cgg gca aca ggg ggg aag atg gcc tac ctc ctc atc gag gag His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu 260 265 270			816

## DI-12

gac atc cgg gac ctc gca gcc agt gat gac tat aga gga tgc ctg gac 864  
 Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp  
           275                          280                          285

ttg aag ttg gag gag ctg aaa tcc ttt gtg ctg ccc tcc tgg atg gtt 912  
 Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val  
           290                          295                          300

gag aag atg cga aag tac atg gag aca cta cgg aca gag aac gag cat 960  
 Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu Asn Glu His  
           305                          310                          315                          320

cgt gct gtt gaa gcg cct cca cag acc 987  
 Arg Ala Val Glu Ala Pro Pro Gln Thr  
                           325

<210> 21  
 <211> 329  
 <212> PRT  
 <213> Canis familiaris

<400> 21

Met Gly Ala Thr Gly Asp Ala Glu Gln Pro Arg Gly Pro Gly Gly Ala  
 1                          5                          10                          15

Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
                           20                          25                          30

Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln  
           35                          40                          45

Arg Arg Gly Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala  
           50                          55                          60

Ile Ser Met Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu  
           65                          70                          75                          80

Glu Ile Gln Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala  
                           85                          90                          95

Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln  
           100                          105                          110

Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu  
           115                          120                          125

Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala His Glu Leu Pro  
           130                          135                          140

DI-12

Gly Ile Lys Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala His Arg Gly  
145 150 155 160

Ser Pro Val Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Met Leu  
165 170 175

Ser Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys  
180 185 190

Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn  
195 200 205

Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly  
210 215 220

Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe  
225 230 235 240

Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His  
245 250 255

His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu  
260 265 270

Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp  
275 280 285

Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val  
290 295 300

Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu Asn Glu His  
305 310 315 320

Arg Ala Val Glu Ala Pro Pro Gln Thr  
325

<210> 22  
<211> 987  
<212> DNA  
<213> Canis familiaris

<400> 22  
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## DI-12

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 caagtccagg catcctctat agtcatcact ggctgcgagg tcccggatgt cctcctcgat 180  
 gaggaggtag gccatcttcc cccctgttgc ccgcatgtga tgctgctcgg ccagccagtg 240  
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 tctggtgccc cccatcccca gggccttggt ggctcgagat cccaacacaa aggtggtaga 360  
 ttcattcagc cgggctgggt cccacttggg gccttctcgg cgaattgggt cacaggactt 420  
 tggtttccat accatgccag cggctgcccg gtcattcgac agcatgtgtc caggaggccg 480  
 tcccttcctc tttttgggaa cagggttcc tcgatgggca cattcctctt ctgtctgtcg 540  
 gccacgcttt atccctggaa gtcctgggc caatctgggt attacttttt ctccatctga 600  
 aaacaggagt ttagcctgct ccaggcagct ccgacaggcc tcctggatca gctgctctgc 660  
 gtccacttct tccccgacat tgtctctgac gttcagtgtc gccttctgga agaacttcat 720  
 atacttggtg aagaccgtct ggatctcctc gttgatgcta ggctgcagga cagctcgaag 780  
 gaggtccatg gaaatggcag gatctgtgaa acttggtgtc atctgtgagc ggcgccccct 840  
 tcgctgcacc tgccgtgtgt ttatcattat gttccaaggg ttcgtgagta ccagctgccc 900  
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 ctgctcggcg tcgccagtgg ccccat 987

<210> 23  
 <211> 153  
 <212> DNA  
 <213> Canis familiaris  
  
 <220>  
 <221> CDS  
 <222> (1)..(153)  
 <223>

<400> 23  
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 1 5 10 15  
  
 gag cgg ggc ggc tcc gag ctg ggc gac gcg ggc gca gcg ggg cag ctg 96  
 Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
 20 25 30  
  
 gta ctc acg aac cct tgg aac ata atg ata aag cac agg cag gtg cag 144  
 Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln  
 35 40 45  
  
 cga agg ggc 153

DI-12

Arg Arg Gly  
50

<210> 24  
<211> 51  
<212> PRT  
<213> Canis familiaris

<400> 24

Met Gly Ala Thr Gly Asp Ala Glu Gln Pro Arg Gly Pro Gly Gly Ala  
1 5 10 15

Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
20 25 30

Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln  
35 40 45

Arg Arg Gly  
50

<210> 25  
<211> 153  
<212> DNA  
<213> Canis familiaris

<400> 25  
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ctgccccgct gcgcccgcgt cgcccagctc ggagccgccc cgctctgccc cgccgggtcc 120  
ccgcggtctgc tcggcgtcgc cagtggcccc cat 153

<210> 26  
<211> 222  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (1)..(222)  
<223>

<400> 26  
cgc cgc tca cag atg aca aca agt ttc aca gat cct gcc att tcc atg 48  
Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala Ile Ser Met  
1 5 10 15  
gac ctc ctt cga gct gtc ctg cag cct agc atc aac gag gag atc cag 96  
Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu Glu Ile Gln



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20	25	30	
acg gtc ttc aac aag tat atg aag ttc ttc cag aag gca gca ctg aac			144
Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala Ala Leu Asn			
35	40	45	
gtc aga gac aat gtc ggg gaa gaa gtg gac gca gag cag ctg atc cag			192
Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln			
50	55	60	
gag gcc tgt cgg agc tgc ctg gag cag gct			222
Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala			
65	70		
<210> 27			
<211> 74			
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<213> Canis familiaris			
<400> 27			
Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala Ile Ser Met			
1	5	10	15
Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu Glu Ile Gln			
20	25	30	
Thr Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala Ala Leu Asn			
35	40	45	
Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln			
50	55	60	
Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala			
65	70		
<210> 28			
<211> 222			
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cccgacattg tctctgacgt tcagtgtgc cttctggaag aacttcatat acttggtgaa			120
gaccgtctgg atctcctcgt tgatgctagg ctgcaggaca gctcgaagga ggtccatgga			180
aatggcagga tctgtgaaac ttgttgcac ctgtgagcgg cg			222
<210> 29			

## DI-12

<211> 612  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(612)  
 <223>

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<400> 29
aaa ctc ctg ttt tca gat gga gaa aaa gta ata ccc aga ttg gcc cat      48
Lys Leu Leu Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala His
1                               5                               10                               15

gag ctt cca ggg ata aag cgt ggc cga cag aca gaa gag gaa tgt gcc      96
Glu Leu Pro Gly Ile Lys Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala
                20                               25                               30

cat cga gga agc cct gtt ccc aaa aag agg aaa gga cgg cct cct gga      144
His Arg Gly Ser Pro Val Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly
                35                               40                               45

cac atg ctg tcg aat gac cgg gca gcc gct ggc atg gta tgg aaa cca      192
His Met Leu Ser Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro
                50                               55                               60

aag tcc tgt gaa cca att cgc cga gaa ggc ccc aag tgg gac cca gcc      240
Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala
65                               70                               75                               80

cgg ctg aat gaa tct acc acc ttt gtg ttg gga tct cga gcc aac aag      288
Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys
                85                               90                               95

gcc ctg ggg atg ggg ggc acc aga ggg aga atc tac atc aag cac ccg      336
Ala Leu Gly Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro
                100                               105                               110

cac ctc ttt aag tat gca gct gac ccc cag gac aag cac tgg ctg gcc      384
His Leu Phe Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala
                115                               120                               125

gag cag cat cac atg cgg gca aca ggg ggg aag atg gcc tac ctc ctc      432
Glu Gln His His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu
                130                               135                               140

atc gag gag gac atc cgg gac ctc gca gcc agt gat gac tat aga gga      480
Ile Glu Glu Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly
145                               150                               155                               160

tgc ctg gac ttg aag ttg gag gag ctg aaa tcc ttt gtg ctg ccc tcc      528
Cys Leu Asp Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser
                165                               170                               175

tgg atg gtt gag aag atg cga aag tac atg gag aca cta cgg aca gag      576
Trp Met Val Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu
                180                               185                               190

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612

aac gag cat cgt gct gtt gaa gcg cct cca cag acc  
Asn Glu His Arg Ala Val Glu Ala Pro Pro Gln Thr  
195 200

<210> 30  
<211> 204  
<212> PRT  
<213> Canis familiaris

<400> 30

Lys Leu Leu Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala His  
1 5 10 15

Glu Leu Pro Gly Ile Lys Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala  
20 25 30

His Arg Gly Ser Pro Val Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly  
35 40 45

His Met Leu Ser Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro  
50 55 60

Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala  
65 70 75 80

Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys  
85 90 95

Ala Leu Gly Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro  
100 105 110

His Leu Phe Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala  
115 120 125

Glu Gln His His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu  
130 135 140

Ile Glu Glu Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly  
145 150 155 160

Cys Leu Asp Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser  
165 170 175

Trp Met Val Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu

180 DI-12 185 190

Asn Glu His Arg Ala Val Glu Ala Pro Pro Gln Thr  
195 200

<210> 31  
<211> 612  
<212> DNA  
<213> Canis familiaris

<400> 31  
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caagtccagg catcctctat agtcatact ggctgagagg tcccgatgt cctcctcgat 180  
gaggaggtag gccatcttcc cccctgttgc ccgcatgtga tgctgctcgg ccagccagtg 240  
cttgctcctgg gggctcagctg cataactaaa gaggtgcggg tgcttgatgt agattctccc 300  
tctggtgccc cccatcccca gggccttggt ggctcgagat cccaacacaa aggtggtaga 360  
ttcattcagc cgggctgggt ccacttggg gccttctcgg cgaattgggt cacaggactt 420  
tggtttccat accatgccag cggctgcccg gtcattcgac agcatgtgtc caggaggccg 480  
tcctttcctc tttttgggaa cagggtctcc tcgatgggca cattcctctt ctgtctgtcg 540  
gccacgcttt atccctggaa gtcatagggc caatctgggt attacttttt ctccatctga 600  
aaacaggagt tt 612

<210> 32  
<211> 96  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (1)..(96)  
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<400> 32  
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Met Gly Ala Thr Gly Asp Ala Glu Gln Pro Arg Gly Pro Gly Gly Ala  
1 5 10 15  
gag cgg ggc ggc tcc gag ctg ggc gac gcg ggc gca gcg ggg cag ctg 96  
Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
20 25 30

<210> 33

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<211> 32  
<212> PRT  
<213> Canis familiaris

<400> 33

Met Gly Ala Thr Gly Asp Ala Glu Gln Pro Arg Gly Pro Gly Gly Ala  
1 5 10 15

Glu Arg Gly Gly Ser Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Leu  
20 25 30

<210> 34  
<211> 96  
<212> DNA  
<213> Canis familiaris

<400> 34  
cagctgcccc gctgagcccc cgctgccccag ctcggagccg ccccgctctg ccccgccggg 60  
tccccgcggc tgctcggcgt cgccagtggc ccccat 96

<210> 35  
<211> 69  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (1)..(69)  
<223>

<400> 35  
aac cct tgg aac ata atg ata aag cac agg cag gtg cag cga agg ggc 48  
Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln Arg Arg Gly  
1 5 10 15  
cgc cgc tca cag atg aca aca 69  
Arg Arg Ser Gln Met Thr Thr  
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<210> 36  
<211> 23  
<212> PRT  
<213> Canis familiaris

<400> 36

Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln Arg Arg Gly  
1 5 10 15

Arg Arg Ser Gln Met Thr Thr

20

<210> 37  
 <211> 69  
 <212> DNA  
 <213> Canis familiaris

<400> 37  
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 ccaagggtt 69

<210> 38  
 <211> 99  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(99)  
 <223>

<400> 38  
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 Ser Phe Thr Asp Pro Ala Ile Ser Met Asp Leu Leu Arg Ala Val Leu  
 1 5 10 15  
 cag cct agc atc aac gag gag atc cag acg gtc ttc aac aag tat atg 96  
 Gln Pro Ser Ile Asn Glu Glu Ile Gln Thr Val Phe Asn Lys Tyr Met  
 20 25 30  
 aag 99  
 Lys

<210> 39  
 <211> 33  
 <212> PRT  
 <213> Canis familiaris

<400> 39  
 Ser Phe Thr Asp Pro Ala Ile Ser Met Asp Leu Leu Arg Ala Val Leu  
 1 5 10 15  
 Gln Pro Ser Ile Asn Glu Glu Ile Gln Thr Val Phe Asn Lys Tyr Met  
 20 25 30  
 Lys

DI-12

<210> 40  
 <211> 99  
 <212> DNA  
 <213> Canis familiaris

<400> 40  
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 tcgaaggagg tccatggaaa tggcaggatc tgtgaaact 99

<210> 41  
 <211> 99  
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<220>  
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 <222> (1)..(99)  
 <223>

<400> 41  
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 Phe Phe Gln Lys Ala Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu  
 1 5 10 15  
 gtg gac gca gag cag ctg atc cag gag gcc tgt cgg agc tgc ctg gag 96  
 Val Asp Ala Glu Gln Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu  
 20 25 30  
 cag 99  
 Gln

<210> 42  
 <211> 33  
 <212> PRT  
 <213> Canis familiaris

<400> 42  
 Phe Phe Gln Lys Ala Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu  
 1 5 10 15  
 Val Asp Ala Glu Gln Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu  
 20 25 30  
 Gln

<210> 43  
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 <212> DNA

DI-12

<213> Canis familiaris

<400> 43  
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gacattgtct ctgacgttca gtgctgcctt ctggaagaa 99

<210> 44  
<211> 69  
<212> DNA  
<213> Canis familiaris

<220>  
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<222> (1)..(69)  
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<400> 44  
gct aaa ctc ctg ttt tca gat gga gaa aaa gta ata ccc aga ttg gcc 48  
Ala Lys Leu Leu Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala  
1 5 10 15

cat gag ctt cca ggg ata aag 69  
His Glu Leu Pro Gly Ile Lys  
20

<210> 45  
<211> 23  
<212> PRT  
<213> Canis familiaris

<400> 45  
Ala Lys Leu Leu Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala  
1 5 10 15

His Glu Leu Pro Gly Ile Lys  
20

<210> 46  
<211> 69  
<212> DNA  
<213> Canis familiaris

<400> 46  
ctttatccct ggaagctcat gggccaatct ggggtattact ttttctccat ctgaaaacag 60

gagtttagc 69

<210> 47  
<211> 57  
<212> DNA



&lt;213&gt; Canis familiaris

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(57)

&lt;223&gt;

&lt;400&gt; 47

cgt ggc cga cag aca gaa gag gaa tgt gcc cat cga gga agc cct gtt 48  
 Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala His Arg Gly Ser Pro Val  
 1 5 10 15

ccc aaa aag

Pro Lys Lys

57

&lt;210&gt; 48

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Canis familiaris

&lt;400&gt; 48

Arg Gly Arg Gln Thr Glu Glu Glu Cys Ala His Arg Gly Ser Pro Val  
 1 5 10 15

Pro Lys Lys

&lt;210&gt; 49

&lt;211&gt; 57

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 49

ctttttggga acagggcttc ctcgatgggc acattcctct tctgtctgtc ggccacg 57

&lt;210&gt; 50

&lt;211&gt; 60

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(60)

&lt;223&gt;

&lt;400&gt; 50

agg aaa gga cgg cct cct gga cac atg ctg tcg aat gac cgg gca gcc 48  
 Arg Lys Gly Arg Pro Pro Gly His Met Leu Ser Asn Asp Arg Ala Ala  
 1 5 10 15

gct ggc atg gta  
Ala Gly Met Val  
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<210> 51  
<211> 20  
<212> PRT  
<213> Canis familiaris

<400> 51

Arg Lys Gly Arg Pro Pro Gly His Met Leu Ser Asn Asp Arg Ala Ala  
1 5 10 15

Ala Gly Met Val  
20

<210> 52  
<211> 60  
<212> DNA  
<213> Canis familiaris

<400> 52  
taccatgcc a gcggtgcc gcc ggtcattcga cagcatgtgt ccaggaggcc gtcctttcct 60

<210> 53  
<211> 45  
<212> DNA  
<213> Canis familiaris

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<221> CDS  
<222> (1)..(45)  
<223>

<400> 53  
tgg aaa cca aag tcc tgt gaa cca att cgc cga gaa ggc ccc aag 45  
Trp Lys Pro Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys  
1 5 10 15

<210> 54  
<211> 15  
<212> PRT  
<213> Canis familiaris

<400> 54

Trp Lys Pro Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys  
1 5 10 15

<210> 55

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<211> 45  
 <212> DNA  
 <213> Canis familiaris

<400> 55  
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45

<210> 56  
 <211> 60  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(60)  
 <223>

<400> 56  
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 Trp Asp Pro Ala Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser  
 1 5 10 15

48

cga gcc aac aag  
 Arg Ala Asn Lys  
 20

60

<210> 57  
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 <212> PRT  
 <213> Canis familiaris

<400> 57  
 Trp Asp Pro Ala Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser  
 1 5 10 15

Arg Ala Asn Lys  
 20

<210> 58  
 <211> 60  
 <212> DNA  
 <213> Canis familiaris

<400> 58  
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60

<210> 59  
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 <212> DNA  
 <213> Canis familiaris

DI-12

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 <223>

<400> 59  
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 Ala Leu Gly Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro  
 1 5 10 15

cac ctc ttt aag 60  
 His Leu Phe Lys  
 20

<210> 60  
 <211> 20  
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 <213> Canis familiaris

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 1 5 10 15

His Leu Phe Lys  
 20

<210> 61  
 <211> 60  
 <212> DNA  
 <213> Canis familiaris

<400> 61  
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<210> 62  
 <211> 72  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(72)  
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<400> 62  
 tat gca gct gac ccc cag gac aag cac tgg ctg gcc gag cag cat cac 48  
 Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His His  
 1 5 10 15

atg cgg gca aca ggg ggg aag atg 72  
 Met Arg Ala Thr Gly Gly Lys Met

20

<210> 63  
 <211> 24  
 <212> PRT  
 <213> Canis familiaris

<400> 63

Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His His  
 1 5 10 15

Met Arg Ala Thr Gly Gly Lys Met  
 20

<210> 64  
 <211> 72  
 <212> DNA  
 <213> Canis familiaris

<400> 64  
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 gtcagctgca ta 72

<210> 65  
 <211> 54  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(54)  
 <223>

<400> 65  
 gcc tac ctc ctc atc gag gag gac atc cgg gac ctc gca gcc agt gat 48  
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 1 5 10 15  
 gac tat 54  
 Asp Tyr

<210> 66  
 <211> 18  
 <212> PRT  
 <213> Canis familiaris

<400> 66

Ala Tyr Leu Leu Ile Glu Glu Asp Ile Arg Asp Leu Ala Ala Ser Asp

Asp Tyr

<210> 67  
 <211> 54  
 <212> DNA  
 <213> Canis familiaris

<400> 67  
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<210> 68  
 <211> 138  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(138)  
 <223>

<400> 68  
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 Arg Gly Cys Leu Asp Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu  
 1 5 10 15

ccc tcc tgg atg gtt gag aag atg cga aag tac atg gag aca cta cgg 96  
 Pro Ser Trp Met Val Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg  
 20 25 30

aca gag aac gag cat cgt gct gtt gaa gcg cct cca cag acc 138  
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 35 40 45

<210> 69  
 <211> 46  
 <212> PRT  
 <213> Canis familiaris

<400> 69  
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 1 5 10 15

Pro Ser Trp Met Val Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg  
 20 25 30

Thr Glu Asn Glu His Arg Ala Val Glu Ala Pro Pro Gln Thr  
 35 40 45

<210> 70  
 <211> 138  
 <212> DNA  
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 caagtccagg catcctct 138

<210> 71  
 <211> 987  
 <212> DNA  
 <213> Canis familiaris

<400> 71  
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 atgataaagc acaggcaagt tcaacgtcgt ggccgccgct cacagatgac aacaagtttc 180  
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 gagatccaga cggctcttcaa caagtatatg aagtctcttc agaaggcagc actgaacgtc 300  
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 tgcctggagc aggctaaact cctgttttca gatggagaaa aagtaatacc cagattggcc 420  
 catgagcttc cagggataaa gcgtggccga cagacagaag aggaatgtgc ccatcgagga 480  
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 aaggccctgg ggatgggggg caccagaggg agaacttaca tcaagcaccg gcacctttt 720  
 aagtatgcag ctgaccccca ggacaagcac tggtggccg agcagcatca catgcgggca 780  
 acagggggga agatggccta cctcctcatc gaggaggaca tccgggacct cgcagccagt 840  
 gatgactata gaggatgcct ggacttgaag ttggaggagc tgaaatcctt tgtgctgccc 900  
 tcctggatgg ttgagaagat gcgaaagtac atggagacac tacggacaga gaacgagcat 960  
 cgtgctgttg aagcgcctcc acagacc 987

<210> 72  
 <211> 987

## DI-12

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 72

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ctttcgcatac ttctcaacca tccaggaggg cagcacaaag gatttcagct cctccaactt      120
caagtccagg catcctctat agtcatcact ggctgcgagg tcccggatgt cctcctcgat      180
gaggaggtag gccatcttcc cccctgttgc ccgcatgtga tgctgctcgg ccagccagtg      240
cttgtcctgg gggtcagctg cataacttaa gaggtgcggg tgcttgatgt agattctccc      300
tctggtgccc cccatcccca gggccttggt ggctcgagat cccaacacaa aggtggtaga      360
ttcattcagc cgggctgggt ccacttggg gccttctcgg cgaattgggt cacaggactt      420
tggtttccat accatgccag cggctgcccg gtcattcgac agcatgtgtc caggaggccg      480
tcctttcctc tttttgggaa cagggttcc tcgatgggca cattcctctt ctgtctgtcg      540
gccacgcttt atccctggaa gtcctgggc caatctgggt attacttttt ctccatctga      600
aaacaggagt ttagcctgct ccaggcagct ccgacaggcc tcctggatca gctgctctgc      660
gtccacttct tccccgacat tgtctctgac gttcagtgtc gccttctgga agaacttcat      720
atacttggtg aagaccgtct ggatctctc gttgatgcta ggctgcagga cagctcgaag      780
gagggtccatg gaaatggcag gatctgtgaa acttggtgtc atctgtgagc ggcgccacg      840
acgttgaact tgcctgtgct ttatcattat gttccaaggg ttcgtgagta ccagctgccc      900
cgctgcgccc gcgtgcccc gctcggagcc gcccgcctct gcccgcctg gacctcttgg      960
ctgctcagcg tcaccagtag caccat                                     987

```

&lt;210&gt; 73

&lt;211&gt; 681

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(681)

&lt;223&gt;

&lt;400&gt; 73

```

aat gtc ggg gaa gaa gtg gac gca gag cag ctg atc cag gag gcc tgt      48
Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln Glu Ala Cys
1          5          10          15

cgg agc tgc ctg gag cag gct aaa ctc ctg ttt tca gat gga gaa aaa      96
Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu Phe Ser Asp Gly Glu Lys
          20          25          30

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## DI-12

gta ata ccc aga ttg gcc cat gag ctt cca ggg ata aag cgt ggc cga 144  
 Val Ile Pro Arg Leu Ala His Glu Leu Pro Gly Ile Lys Arg Gly Arg  
 35 40 45

cag aca gaa gag gaa tgt gcc cat cga gga agc cct gtt ccc aaa aag 192  
 Gln Thr Glu Glu Glu Cys Ala His Arg Gly Ser Pro Val Pro Lys Lys  
 50 55 60

agg aaa gga cgg cct cct gga cac atg ctg tgc aat gac cgg gca gcc 240  
 Arg Lys Gly Arg Pro Pro Gly His Met Leu Ser Asn Asp Arg Ala Ala  
 65 70 75 80

gct ggc atg gta tgg aaa cca aag tcc tgt gaa cca att cgc cga gaa 288  
 Ala Gly Met Val Trp Lys Pro Lys Ser Cys Glu Pro Ile Arg Arg Glu  
 85 90 95

ggc ccc aag tgg gac cca gcc cgg ctg aat gaa tct acc acc ttt gtg 336  
 Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn Glu Ser Thr Thr Phe Val  
 100 105 110

ttg gga tct cga gcc aac aag gcc ctg ggg atg ggg ggc acc aga ggg 384  
 Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly Met Gly Gly Thr Arg Gly  
 115 120 125

aga atc tac atc aag cac ccg cac ctc ttt aag tat gca gct gac ccc 432  
 Arg Ile Tyr Ile Lys His Pro His Leu Phe Lys Tyr Ala Ala Asp Pro  
 130 135 140

cag gac aag cac tgg ctg gcc gag cag cat cac atg cgg gca aca ggg 480  
 Gln Asp Lys His Trp Leu Ala Glu Gln His His Met Arg Ala Thr Gly  
 145 150 155 160

ggg aag atg gcc tac ctc ctc atc gag gag gac atc cgg gac ctc gca 528  
 Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu Asp Ile Arg Asp Leu Ala  
 165 170 175

gcc agt gat gac tat aga gga tgc ctg gac ttg aag ttg gag gag ctg 576  
 Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp Leu Lys Leu Glu Glu Leu  
 180 185 190

aaa tcc ttt gtg ctg ccc tcc tgg atg gtt gag aag atg cga aag tac 624  
 Lys Ser Phe Val Leu Pro Ser Trp Met Val Glu Lys Met Arg Lys Tyr  
 195 200 205

atg gag aca cta cgg aca gag aac gag cat cgt gct gtt gaa gcg cct 672  
 Met Glu Thr Leu Arg Thr Glu Asn Glu His Arg Ala Val Glu Ala Pro  
 210 215 220

cca cag acc 681  
 Pro Gln Thr  
 225

<210> 74  
 <211> 227  
 <212> PRT  
 <213> Canis familiaris

## DI-12

&lt;400&gt; 74

Asn Val Gly Glu Glu Val Asp Ala Glu Gln Leu Ile Gln Glu Ala Cys  
 1 5 10 15

Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu Phe Ser Asp Gly Glu Lys  
 20 25 30

Val Ile Pro Arg Leu Ala His Glu Leu Pro Gly Ile Lys Arg Gly Arg  
 35 40 45

Gln Thr Glu Glu Glu Cys Ala His Arg Gly Ser Pro Val Pro Lys Lys  
 50 55 60

Arg Lys Gly Arg Pro Pro Gly His Met Leu Ser Asn Asp Arg Ala Ala  
 65 70 75 80

Ala Gly Met Val Trp Lys Pro Lys Ser Cys Glu Pro Ile Arg Arg Glu  
 85 90 95

Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn Glu Ser Thr Thr Phe Val  
 100 105 110

Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly Met Gly Gly Thr Arg Gly  
 115 120 125

Arg Ile Tyr Ile Lys His Pro His Leu Phe Lys Tyr Ala Ala Asp Pro  
 130 135 140

Gln Asp Lys His Trp Leu Ala Glu Gln His His Met Arg Ala Thr Gly  
 145 150 155 160

Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu Asp Ile Arg Asp Leu Ala  
 165 170 175

Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp Leu Lys Leu Glu Glu Leu  
 180 185 190

Lys Ser Phe Val Leu Pro Ser Trp Met Val Glu Lys Met Arg Lys Tyr  
 195 200 205

Met Glu Thr Leu Arg Thr Glu Asn Glu His Arg Ala Val Glu Ala Pro  
 210 215 220

Pro Gln Thr  
225

<210> 75  
<211> 681  
<212> DNA  
<213> Canis familiaris

<400> 75  
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ctttcgcata ttctcaacca tccaggaggg cagcaciaag gatttcagct cctccaactt 120  
caagtccagg catcctctat agtcatcact ggctgagagg tcccggatgt cctcctcgat 180  
gaggaggtag gccatcttcc cccctgttgc ccgcatgtga tgctgctcgg ccagccagtg 240  
cttgtcctgg gggtcagctg cataactaaa gaggtgcggg tgcttgatgt agattctccc 300  
tctggtgccc cccatcccca gggccttggt ggctcgagat cccaacacaa agtggtgtaga 360  
ttcattcagc cgggctgggt cccacttggg gccttctcgg cgaattgggt cacaggactt 420  
tggtttccat accatgccag cggctgcccg gtcattcgac agcatgtgtc caggaggccg 480  
tcctttcctc tttttgggaa cagggcttcc tcgatgggca cattcctctt ctgtctgtcg 540  
gccacgcttt atccctggaa gtcctatggg caatctgggt attacttttt ctccatctga 600  
aaacaggagt ttagcctgct ccaggcagct ccgacaggcc tcttgatca gctgctctgc 660  
gtccacttct tccccgacat t 681

<210> 76  
<211> 681  
<212> DNA  
<213> Canis familiaris

<400> 76  
aacgttggtg aagaagtgga cgcagagcag ctgatccagg aggcctgtcg gagctgcctg 60  
gagcaggcta aactcctggt ttcagatgga gaaaaagtaa taccagatt ggcccatgag 120  
cttccaggga taaagcgtgg ccgacagaca gaagaggaat gtgcccatcg aggaagccct 180  
gttcccaaaa agaggaaagg acggcctcct ggacacatgc tgtcgaatga ccgggcagcc 240  
gctggcatgg tatggaaacc aaagtctgt gaaccaattc gccgagaagg cccaagtgg 300  
gaccagccc ggctgaatga atctaccacc tttgtgttgg gatctcgagc caacaaggcc 360  
ctggggatgg ggggcaccag agggagaatc tacatcaagc acccgcacct ctttaagtat 420  
gcagctgacc cccaggacaa gactggctg gccgagcagc atcacatgcg ggcaacaggg 480

DI-12

gggaagatgg cctacctoct catcgaggag gacatccggg acctcgcagc cagtgatgac 540  
tatagaggat gcctggactt gaagttggag gagctgaaat cctttgtgct gccctcctgg 600  
atggttgaga agatgcgaaa gtacatggag acactacgga cagagaacga gcatcgtgct 660  
gttgaagcgc ctccacagac c 681

<210> 77  
<211> 681  
<212> DNA  
<213> Canis familiaris

<400> 77  
ggtctgtgga ggcgcttcaa cagcacgatg ctggttctct gtccgtagtg tctccatgta 60  
ctttcgcata ttctcaacca tccaggaggg cagcacaag gatttcagct cctccaactt 120  
caagtccagg catcctctat agtcatcact ggctgcgagg tcccggatgt cctcctcgat 180  
gaggaggtag gccatcttcc cccctgttgc ccgcatgtga tgctgctcgg ccagccagtg 240  
cttgtcctgg gggtcagctg cataacttaa gaggtgcggg tgcttgatgt agattctccc 300  
tctggtgccc cccatcccca gggccttgtt ggctcgagat cccaacacaa aggtggtaga 360  
ttcattcagc cgggctgggt cccacttggg gccttctcgg cgaattgggt cacaggactt 420  
tggtttccat accatgccag cggctgccc gtcattcgac agcatgtgtc caggaggccg 480  
tcctttcctc tttttgggaa cagggttcc tcgatgggca cattcctctt ctgtctgtcg 540  
gccacgcttt atccctggaa gtcatgggc caatctgggt attacttttt ctccatctga 600  
aaacaggagt ttagcctgct ccaggcagct ccgacaggcc tcctggatca gctgctctgc 660  
gtccacttct tcaccaacgt t 681

<210> 78  
<211> 54  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic Primer

<400> 78  
gttaaacata tgggtgctac tggtgacgt gagcagccaa gaggtccagg cggg 54

<210> 79  
<211> 39  
<212> DNA  
<213> Artificial sequence

<220>

DI-12

<223> Synthetic Primer

<400> 79  
gcggcgccca cgacgttgaa cttgcctgtg ctttatcat

39

<210> 80  
<211> 39  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic Primer

<400> 80  
atgataaagc acaggcaagt tcaacgtcgt ggccgccgc

39

<210> 81  
<211> 30  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic Primer

<400> 81  
atgcacgaat tctcaggtct gtggaggcgc

30

<210> 82  
<211> 33  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic Primer

<400> 82  
gttaaacata tgggtgctac tgggtgacgct gag

33

<210> 83  
<211> 27  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Synthetic Primer

<400> 83  
atgcacgaat tctcaggtct gtggagg

27

<210> 84  
<211> 45  
<212> DNA  
<213> Artificial sequence

DI-12

<220>

<223> Synthetic Primer

<400> 84

gcgaattccc atatgaacgt tggatgaagaa gtggacgcag agcag

45

<210> 85

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic Primer

<400> 85

cgtcttgaa ttctcaggtc tggaggcg cttcaac

37

DI-12